

PCT

RAW SEQUENCE LISTING DATE: 12/26/2000
 PATENT APPLICATION: US/09/673,198 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
 Output Set: N:\CRF3\12262000\I673198.raw

**Does Not Comply
 Corrected Diskette Needed**

2 <110> APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOYOYAMA Hiroaki;
 3 OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
 5 <120> TITLE OF INVENTION: A process for producing isoprenoid compounds by
 6 microorganisms and a method for screening compounds with
 7 antibiotic or weeding activity
 W--> 9 <130> FILE REFERENCE:
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,198
 C--> 12 <141> CURRENT FILING DATE: 2000-10-12
 14 <150> PRIOR APPLICATION NUMBER: JP98/103101
 15 <151> PRIOR FILING DATE: 1998-04-14
 17 <150> PRIOR APPLICATION NUMBER: JP98/221910
 18 <151> PRIOR FILING DATE: 1998-08-05
 20 <150> PRIOR APPLICATION NUMBER: JP99/035739
 21 <151> PRIOR FILING DATE: 1999-02-15
 23 <160> NUMBER OF SEQ ID NOS: 34
 25 <170> SOFTWARE: PatentIn Ver. 2.0

BEST AVAILABLE COPY

ERRORED SEQUENCES

392 <210> SEQ ID NO: 6
 393 <211> LENGTH: 1860
 394 <212> TYPE: DNA
 395 <213> ORGANISM: Escherichia coli
 397 <220> FEATURE:
 398 <221> NAME/KEY: CDS
 399 <222> LOCATION: (1)..(1860)
 401 <400> SEQUENCE: 6
 E--> 402 atg agt ttt gat att gcc aaa tac ccg acc ctg gca ctg gtc gac tcc
 403 48
 405 Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser
 406 1 5 10 15
 E--> 408 acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc
 409 96
 411 Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys
 412 20 25 30
 E--> 414 gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg
 415 144
 417 Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly
 418 35 40 45
 E--> 420 cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac
 421 192
 423 His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His
 424 50 55 60
 E--> 426 tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat
 427 240
 429 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His

format error

→ 48

↓

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```

      130   65              70              75              80
E--> 432 cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc
      433 288
      435 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly
      436              85              90              95
E--> 438 acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa
      439 336
      441 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu
      442              100              105              110
E--> 444 agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt
      445 384
      447 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser
      448              115              120              125
E--> 450 gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc
      451 432
      453 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg
      454              130              135              140
E--> 456 cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcg
      457 480
      459 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala
      460 145              150              155              160
E--> 462 ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg
      463 528
      465 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val
      466              165              170              175
E--> 468 att ctc aac gac aat gaa atg tcg att tcc gaa aat gtc ggc gcg ctc
      469 576
      471 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu
      472              180              185              190
E--> 474 aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg
      475 624
      477 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu
      478              195              200              205
E--> 480 cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccg cca att aaa gag
      481 672
      483 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu
      484              210              215              220
E--> 486 ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc
      487 720
      489 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly
      490 225              230              235              240
E--> 492 acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccg gtg gac ggt
      493 768
      495 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly
      496              245              250              255
E--> 498 cac gat gtg ctg ggg ctt atc acc acg cta aag aac atg cgc gac ctg
      499 816
      501 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu
      502              260              265              270

```

same

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```

E--> 504 aaa ggc ccg cag ttc ctg cat atc atg acc aaa aaa ggt cgt ggt tat
      505 864
      507 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr
      508      275      280      285
E--> 510 gaa ccg gca gaa aaa gac ccg atc act ttc cac gcc gtg cct aaa ttt
      511 912
      513 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe
      514      290      295      300
E--> 516 gat ccc tcc agc ggt tgt ttg ccg aaa agt agc ggc ggt ttg ccg agc
      517 960
      519 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser
      520      305      310      315      320
E--> 522 tat tca aaa atc ttt ggc gac tgg ttg tgc gaa acg gca gcg aaa gac
      523 1008
      525 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp
      526      325      330      335
E--> 528 aac aag ctg atg gcg att act ccg gcg atg cgt gaa ggt tcc ggc atg
      529 1056
      531 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met
      532      340      345      350
E--> 534 gtc gag ttt tca cgt aaa ttc ccg gat cgc tac ttc gac gtg gca att
      535 1104
      537 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile
      538      355      360      365
E--> 540 gcc gag caa cac gcg gtg acc ttt gct gcg ggt ctg gcg att ggt ggg
      541 1152
      543 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly
      544      370      375      380
E--> 546 tac aaa ccc att gtc gcg att tac tcc act ttc ctg caa cgc gcc tat
      547 1200
      549 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr
      550      385      390      395      400
E--> 552 gat cag gtg ctg cat gac gtg gcg att caa aag ctt ccg gtc ctg ttc
      553 1248
      555 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe
      556      405      410      415
E--> 558 gcc atc gac cgc gcg ggc att gtt ggt gct gac ggt caa acc cat cag
      559 1296
      561 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln
      562      420      425      430
E--> 564 ggt gct ttt gat ctc tct tac ctg cgc tgc ata ccg gaa atg gtc att
      565 1344
      567 Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile
      568      435      440      445
E--> 570 atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc
      571 1392
      573 Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly
      574      450      455      460
E--> 576 tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac

```

same

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```

577 1440
579 Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn
580 465 470 475 480
E--> 582 gcg gtc ggc gtg gaa ctg acg ccg ctg gaa aaa cta cca att ggc aaa
583 1488
585 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys
586 485 490 495
E--> 588 ggc att gtg aag cgt cgt ggc gag aaa ctg gcg atc ctt aac ttt ggt
589 1536
591 Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly
592 500 505 510
E--> 594 acg ctg atg cca gaa gcg gcg aaa gtc gcc gaa tcg ctg aac gcc acg
595 1584
597 Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr
598 515 520 525
E--> 600 ctg gtc gat atg cgt ttt gtg aaa ccg ctt gat gaa gcg tta att ctg
601 1632
603 Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu
604 530 535 540
E--> 606 gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc
607 1680
609 Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala
610 545 550 555 560
E--> 612 att atg ggc ggc gca ggc agc ggc gtg aac gaa gtg ctg atg gcc cat
613 1728
615 Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His
616 565 570 575
E--> 618 cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att
619 1776
621 Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile
622 580 585 590
E--> 624 ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc
625 1824
627 Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala
628 595 600 605
E--> 630 gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca
631 1860
633 Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala
634 610 615 620
637 <210> SEQ ID NO: 7
638 <211> LENGTH: 897
639 <212> TYPE: DNA
640 <213> ORGANISM: Escherichia coli
642 <220> FEATURE:
643 <221> NAME/KEY: CDS
644 <222> LOCATION: (1)..(897)
646 <400> SEQUENCE: 7
E--> 647 atg gac ttt ccg cag caa ctc gaa gcc tgc gtt aag cag gcc aac cag
648 48

```

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```

650 Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln
651 1 5 10 15
E--> 653 gcg ctg agc cgt ttt atc gcc cca ctg ccc ttt cag aac act ccc gtg
654 96
656 Ala Leu Ser Arg Phe Ile Ala Pro Leu Pro Phe Gln Asn Thr Pro Val
657 20 25 30
E--> 659 gtc gaa acc atg cag tat ggc gca tta tta ggt ggt aag cgc ctg cga
660 144
662 Val Glu Thr Met Gln Tyr Gly Ala Leu Leu Gly Gly Lys Arg Leu Arg
663 35 40 45
E--> 665 cct ttc ctg gtt tat gcc acc ggt cat atg ttc ggc gtt agc aca aac
666 192
668 Pro Phe Leu Val Tyr Ala Thr Gly His Met Phe Gly Val Ser Thr Asn
669 50 55 60
E--> 671 acg ctg gac gca ccc gct gcc gcc gtt gag tgt atc cac gct tac tca
672 240
674 Thr Leu Asp Ala Pro Ala Ala Val Glu Cys Ile His Ala Tyr Ser
675 65 70 75 80
E--> 677 tta att cat gat gat tta ccg gca atg gat gat gac gat ctg cgt cgc
678 288
680 Leu Ile His Asp Asp Leu Pro Ala Met Asp Asp Asp Leu Arg Arg
681 85 90 95
E--> 683 ggt ttg cca acc tgc cat gtg aag ttt ggc gaa gca aac gcg att ctc
684 336
686 Gly Leu Pro Thr Cys His Val Lys Phe Gly Glu Ala Asn Ala Ile Leu
687 100 105 110
E--> 689 gct ggc gac gct tta caa acg ctg gcg ttc tcg att tta agc gat gcc
690 384
692 Ala Gly Asp Ala Leu Gln Thr Leu Ala Phe Ser Ile Leu Ser Asp Ala
693 115 120 125
E--> 695 gat atg ccg gaa gtg tcg gac cgc gac aga att tcg atg att tct gaa
696 432
698 Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu
699 130 135 140
E--> 701 ctg gcg agc gcc agt ggt att gcc gga atg tgc ggt ggt cag gca tta
702 480
704 Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu
705 145 150 155 160
E--> 707 gat tta gac gcg gaa ggc aaa cac gta cct ctg gac gcg ctt gag cgt
708 528
710 Asp Leu Asp Ala Glu Gly Lys His Val Pro Leu Asp Ala Leu Glu Arg
711 165 170 175
E--> 713 att cat cgt cat aaa acc ggc gca ttg att cgc gcc gcc gtt cgc ctt
714 576
716 Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu
717 180 185 190
E--> 719 ggt gca tta agc gcc gga gat aaa gga cgt cgt gct ctg ccg gta ctc
720 624
722 Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu

```

same

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```

723      195      200      205
E--> 725 gac aag tat gca gag agc atc ggc ctt gcc ttc cag gtt cag gat gac
726 672
728 Asp Lys Tyr Ala Glu Ser Ile Gly Leu Ala Phe Gln Val Gln Asp Asp
729      210      215      220
E--> 731 atc ctg gat gtg gtg gga gat act gca acg ttg gga aaa cgc cag ggt
732 720
734 Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly
735 225      230      235      240
E--> 737 gcc gac cag caa ctt ggt aaa agt acc tac cct gca ctt ctg ggt ctt
738 768
740 Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu
741      245      250      255
E--> 743 gag caa gcc cgg aag aaa gcc cgg gat ctg atc gac gat gcc cgt cag
744 816
746 Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln
747      260      265      270
E--> 749 tcg ctg aaa caa ctg gct gaa cag tca ctc gat acc tcg gca ctg gaa
750 864
752 Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu
753      275      280      285
E--> 755 gcg cta gcg gac tac atc atc cag cgt aat aaa
756 897
758 Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys
759      290      295
762 <210> SEQ ID NO: 8
763 <211> LENGTH: 240
764 <212> TYPE: DNA
765 <213> ORGANISM: Escherichia coli
766 <220> FEATURE:
767 <221> NAME/KEY: CDS
768 <222> LOCATION: (1)..(240)
771 <400> SEQUENCE: 8
E--> 772 atg ccg aag aaa aat gag gcg ccc gcc agc ttt gaa aag gcg ctg agc
773 48
775 Met Pro Lys Lys Asn Glu Ala Pro Ala Ser Phe Glu Lys Ala Leu Ser
776      1      5      10      15
E--> 778 gag ctg gaa cag att gta acc cgt ctg gaa agt ggc gac ctg ccg ctg
779 96
781 Glu Leu Glu Gln Ile Val Thr Arg Leu Glu Ser Gly Asp Leu Pro Leu
782      20      25      30
E--> 784 gaa gag gcg ctg aac gag ttc gaa cgc ggc gtg cag ctg gca cgt cag
785 144
787 Glu Gln Ala Leu Asn Glu Phe Glu Arg Gly Val Gln Leu Ala Arg Gln
788      35      40      45
E--> 790 ggg cag gcc aaa tta caa caa gcc gaa cag cgc gta caa att ctg ctg
791 192
793 Gly Gln Ala Lys Leu Gln Gln Ala Glu Gln Arg Val Gln Ile Leu Leu
794      50      55      60

```

same

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```

E--> 796 tct gac aat gaa gac gcc tct cta acc cct ttt aca ccg gac aat gag
      797 240
      799 Ser Asp Asn Glu Asp Ala Ser Leu Thr Pro Phe Thr Pro Asp Asn Glu
      800 65 70 75 80
      803 <210> SEQ ID NO: 9
      804 <211> LENGTH: 1044
      805 <212> TYPE: DNA
      806 <213> ORGANISM: Escherichia coli
      808 <220> FEATURE:
      809 <221> NAME/KEY: CDS
      810 <222> LOCATION: (1)..(1044)
      812 <400> SEQUENCE: 9
E--> 813 gtg act ggg gtg aac gaa tgc agc cgc agc aca tgc aac ttg aag tat
      814 48
      816 Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr Cys Asn Leu Lys Tyr
      817 1 5 10 15
E--> 819 gac gag tat agc agg agt ggc agc atg caa tac aac ccc tta gga aaa
      820 96
      822 Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr Asn Pro Leu Gly Lys
      823 20 25 30
E--> 825 acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc tgt atg acc ttt ggc
      826 144
      828 Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly Cys Met Thr Phe Gly
      829 35 40 45
E--> 831 gag cca gat cgc ggt aat cac gca tgg aca ctg ccg gaa gaa agc agc
      832 192
      834 Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu Pro Glu Glu Ser Ser
      835 50 55 60
E--> 837 cgt ccc ata att aaa cgt gca ctg gaa ggc ggc ata aat ttc ttt gat
      838 240
      840 Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly Ile Asn Phe Phe Asp
      841 65 70 75 80
E--> 843 acc gcc aac agt tat tct gac ggc agc agc gaa gag atc gtc ggt cgc
      844 288
      846 Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu Glu Ile Val Gly Arg
      847 85 90 95
E--> 849 gca ctg egg gat ttc gcc cgt cgt gaa gac gtg gtc gtt gcg acc aaa
      850 336
      852 Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val Val Val Ala Thr Lys
      853 100 105 110
E--> 855 gtg ttc cat cgc gtt ggt gat tta ccg gaa gga tta tcc cgt gcg caa
      856 384
      858 Val Phe His Arg Val Gly Asp Leu Pro Glu Gly Leu Ser Arg Ala Gln
      859 115 120 125
E--> 861 att ttg cgc tct atc gac gac agc ctg cga cgt ctc ggc atg gat tat
      862 432
      864 Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg Leu Gly Met Asp Tyr
      865 130 135 140
E--> 867 gtc gat atc ctg caa att cat cgc tgg gat tac aac acg ccg atc gaa

```

same

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```

868 480
870 Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr Asn Thr Pro Ile Glu
871 145 150 155 160
E--> 873 gag acg ctg gaa gcc ctc aac gac gtg gta aaa gcc ggg aaa gcg cgt
874 528
876 Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys Ala Gly Lys Ala Arg
877 165 170 175
E--> 879 tat atc ggc gcg tca tca atg cac gct tgg cag ttt gct cag gca ctg
880 576
882 Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln Phe Ala Gln Ala Leu
883 180 185 190
E--> 885 gaa ctc caa aaa cag cac ggc tgg gcg cag ttt gtc agt atg cag gat
886 624
888 Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe Val Ser Met Gln Asp
889 195 200 205
E--> 891 cac tac aat ctg att tat cgt gaa gaa gag cgc gag atg cta cca ctg
892 672
894 His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg Glu Met Leu Pro Leu
895 210 215 220
E--> 897 tgt tat cag gag ggc gtg gcg gta att cca tgg agc ccg ctg gca agg
898 720
900 Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp Ser Pro Leu Ala Arg
901 225 230 235 240
E--> 903 ggc cgt ctg acg cgt ccg tgg gga gaa act acc gca cga ctg gtg tct
904 768
906 Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr Ala Arg Leu Val Ser
907 245 250 255
E--> 909 gat gag gtg ggg aaa aat ctc tat aaa gaa agc gat gaa aat gac gcg
910 816
912 Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser Asp Glu Asn Asp Ala
913 260 265 270
E--> 915 cag atc gca gag cgg tta aca ggc gtc agt gaa gaa ctg ggg gcg aca
916 864
918 Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu Glu Leu Gly Ala Thr
919 275 280 285
E--> 921 cga gca caa gtt gcg ctg gcc tgg ttg ttg agt aaa ccg ggc att gcc
922 912
924 Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser Lys Pro Gly Ile Ala
925 290 295 300
E--> 927 gca ccg att atc gga act tgg cgc gaa gaa cag ctt gat gag cta ttg
928 960
930 Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln Leu Asp Glu Leu Leu
931 305 310 315 320
E--> 933 aac gcg gtg gat atc act ttg aag ccg gaa cag att gcc gaa ctg gaa
934 1008
936 Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln Ile Ala Glu Leu Glu
937 325 330 335
E--> 939 acg ccg tat aaa ccg cat cct gtc gta gga ttt aaa
940 1044

```

same

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```

942 Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe Lys
943                               340           345
946 <210> SEQ ID NO: 10
947 <211> LENGTH: 1194
948 <212> TYPE: DNA
949 <213> ORGANISM: Escherichia coli
951 <220> FEATURE:
952 <221> NAME/KEY: CDS
953 <222> LOCATION: (1)..(1194)
955 <400> SEQUENCE: 10
E--> 956 atg aag caa ctc acc att ctg ggc tcg acc ggc tcg att ggt tgc agc
957 48
959 Met Lys Gln Leu Thr Ile Leu Gly Ser Thr Gly Ser Ile Gly Cys Ser
960 1 5 10 15
E--> 962 acg ctg gac gtg gtg cgc cat aat ccc gaa cac ttc cgc gta gtt gcg
963 96
965 Thr Leu Asp Val Val Arg His Asn Pro Glu His Phe Arg Val Val Ala
966 20 25 30
E--> 968 ctg gtg gca ggc aaa aat gtc act cgc atg gta gaa cag tgc ctg gaa
969 144
971 Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu
972 35 40 45
E--> 974 ttc tct ccc cgc tat gcc gta atg gac gat gaa gcg agt gcg aaa ctt
975 192
977 Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu
978 50 55 60
E--> 980 ctt aaa acg atg cta cag caa cag ggt agc cgc acc gaa gtc tta agt
981 240
983 Leu Lys Thr Met Leu Gln Gln Gln Gly Ser Arg Thr Glu Val Leu Ser
984 65 70 75 80
E--> 986 ggg caa caa gcc gct tgc gat atg gca gcg ctt gag gat gtt gat cag
987 288
989 Gly Gln Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln
990 85 90 95
E--> 992 gtg atg gca gcc att gtt ggc gct gct ggg ctg tta cct acg ctt gct
993 336
995 Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala
996 100 105 110
E--> 998 gcg atc cgc gcg ggt aaa acc att ttg ctg gcc aat aaa gaa tca ctg
999 384
1001 Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu
1002 115 120 125
E--> 1004 gtt acc tgc gga cgt ctg ttt atg gac gcc gta aag cag agc aaa gcg
1005 432
1007 Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala
1008 130 135 140
E--> 1010 caa ttg tta ccg gtc gat agc gaa cat aac gcc att ttt cag agt tta
1011 480
1013 Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu

```

same

RAW SEQUENCE LISTING

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

```

1014 145          150          155          160
E--> 1016 ccg caa cct atc cag cat aat ctg gga tac gct gac ctt gag caa aat
1017 528
1019 Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn
1020          165          170          175
E--> 1022 ggc gtg gtg tcc att tta ctt acc ggg tct ggt ggc cct ttc cgt gag
1023 576
1025 Gly Val Val Ser Ile Leu Leu Thr Gly Ser Gly Gly Pro Phe Arg Glu
1026          180          185          190
E--> 1028 acg cca ttg cgc gat ttg gca aca atg acg ccg gat caa gcc tgc cgt
1029 624
1031 Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg
1032          195          200          205
E--> 1034 cat ccg aac tgg tgc atg ggg cgt aaa att tct gtc gat tgc gct acc
1035 672
1037 His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr
1038          210          215          220
E--> 1040 atg atg aac aaa ggt ctg gaa tac att gaa gcg cgt tgg ctg ttt aac
1041 720
1043 Met Met Asn Lys Gly Leu Glu Tyr Ile Glu Ala Arg Trp Leu Phe Asn
1044 225          230          235          240
E--> 1046 gcc agc gcc agc cag atg gaa gtg ctg att cac ccg cag tca gtg att
1047 768
1049 Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile
1050          245          250          255
E--> 1052 cac tca atg gtg cgc tat cag gac ggc agt gtt ctg gcg cag ctg ggg
1053 816
1054 His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly
1055          260          265          270
E--> 1057 gaa ccg gat atg gta cgc caa ttg ccc aca cca tgg gca tgg ccg aat
1058 864
1060 Glu Pro Asp Met Val Arg Gln Leu Pro Thr Pro Trp Ala Trp Pro Asn
1061          275          280          285
E--> 1063 cgc gtg aac tct ggc gtg aag ccg ctc gat ttt tgc aaa cta agt gcg
1064 912
1066 Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala
1067          290          295          300
E--> 1069 ttg aca ttt gcc gca ccg gat tat gat cgt tat cca tgc ctg aaa ctg
1070 960
1072 Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu
1073 305          310          315          320
E--> 1075 gcg atg gag gcg ttc gaa caa ggc cag gca gcg acg aca gca ttg aat
1076 1008
1078 Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn
1079          325          330          335
E--> 1081 gcc gca aac gaa atc acc gtt gct gct ttt ctt gcg caa caa atc cgc
1082 1056
1084 Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg
1085          340          345          350

```

Name

RAW SEQUENCE LISTING DATE: 12/26/2000
 PATENT APPLICATION: US/09/673,198 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
 Output Set: N:\CRF3\12262000\I673198.raw

```

E--> 1087 ttt acg gat atc gct gcg ttg aat tta tcc gta ctg gaa aaa atg gat
      1088 1104
      1090 Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp
      1091          355          360          365
E--> 1093 atg cgc gaa cca caa tgt gtg gac gat gtg tta tct gtt gat gcg aac
      1094 1152
      1096 Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn
      1097          370          375          380
E--> 1099 gcg cgt gaa gtc gcc aga aaa gag gtg atg cgt ctc gca agc
      1100 1194
      1102 Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser
      1103 385          390          395
      1106 <210> SEQ ID NO: 11
      1107 <211> LENGTH: 4390
      1108 <212> TYPE: DNA
      1109 <213> ORGANISM: Escherichia coli
      1111 <220> FEATURE:
      1112 <221> NAME/KEY: CDS
      1113 <222> LOCATION: (208)..(447)
      1115 <220> FEATURE:
      1116 <221> NAME/KEY: CDS
      1117 <222> LOCATION: (450)..(1346)
      1119 <220> FEATURE:
      1120 <221> NAME/KEY: CDS
      1121 <222> LOCATION: (1374)..(3233)
      1123 <220> FEATURE:
      1124 <221> NAME/KEY: CDS
      1125 <222> LOCATION: (3344)..(4390)
      1127 <400> SEQUENCE: 11
E--> 1128 atggcgggcaa tgggttcgttg gcaagcctta agcgacttgt atagggaaaa atacagcagc
      1129 60
E--> 1132 ccacacctgc ggctgcatcc aggcgcggaa gtataccact aacatcgctt tgctgtgcac
      1133 120
E--> 1136 atcaccttac cattgcgcgt tatttgctat ttgccctgag tccgttacca tgacggggcg
      1137 180
E--> 1140 aaaaatattg agagtcagac attcatt atg ccg aag aaa aat gag gcg ccc gcc
      1141 234
      1143 Met. Pro Lys Lys Asn Glu Ala Pro Ala
      1144          1          5
E--> 1146 agc ttt gaa aag gcg ctg agc gag ctg gaa cag att gta acc cgt ctg
      1147 282
      1149 Ser Phe Glu Lys Ala Leu Ser Glu Leu Glu Gln Ile Val Thr Arg Leu
      1150 10          15          20          25
E--> 1152 gaa agt ggc gac ctg ccg ctg gaa gag gcg ctg aac gag ttc gaa cgc
      1153 330
      1155 Glu Ser Gly Asp Leu Pro Leu Glu Glu Ala Leu Asn Glu Phe Glu Arg
      1156          30          35          40
E--> 1158 ggc gtg cag ctg gca cgt cag ggg cag gcc aaa tta caa caa gcc gaa
      1159 378

```

same

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,198

DATE: 12/26/2000

TIME: 13:19:35

Input Set : A:\1241.16\sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

```

1161 Gly Val Gln Leu Ala Arg Gln Gly Gln Ala Lys Leu Gln Gln Ala Glu
1162          45          50          55
E--> 1164 cag cgc gta caa att ctg ctg tct gac aat gaa gac gcc tct cta acc
1165 426
1167 Gln Arg Val Gln Ile Leu Leu Ser Asp Asn Glu Asp Ala Ser Leu Thr
1168          60          65          70
E--> 1170 cct ttt aca ccg gac aat gag ta atg gac ttt ccg cag caa ctc gaa
1171 473
W--> 1173 Pro Phe Thr Pro Asp Asn Glu Met Asp Phe Pro Gln Gln Leu Glu
W--> 1174          75          80          1          5
E--> 1176 gcc tgc gtt aag cag gcc aac cag gcg ctg agc cgt ttt atc gcc cca
1177 521
1179 Ala Cys Val Lys Gln Ala Asn Gln Ala Leu Ser Arg Phe Ile Ala Pro
W--> 1180          10          15          20
E--> 1182 ctg ccc ttt cag aac act ccc gtg gtc gaa acc atg cag tat ggc gca
1183 569
1185 Leu Pro Phe Gln Asn Thr Pro Val Val Glu Thr Met Gln Tyr Gly Ala
W--> 1186          25          30          35          40
E--> 1188 tta tta ggt ggt aag cgc ctg cga cct ttc ctg gtt tat gcc acc ggt
1189 617
1191 Leu Leu Gly Gly Lys Arg Leu Arg Pro Phe Leu Val Tyr Ala Thr Gly
W--> 1192          45          50          55
E--> 1194 cat atg ttc ggc gtt agc aca aac acg ctg gac gca ccc gct gcc gcc
1195 665
1197 His Met Phe Gly Val Ser Thr Asn Thr Leu Asp Ala Pro Ala Ala Ala
W--> 1198          60          65          70
E--> 1200 gtt gag tgt atc cac gct tac tca tta att cat gat gat tta ccg gca
1201 713
1203 Val Glu Cys Ile His Ala Tyr Ser Leu Ile His Asp Asp Leu Pro Ala
W--> 1204          75          80          85
E--> 1206 atg gat gat gac gat ctg cgt cgc ggt ttg cca acc tgc cat gtg aag
1207 761
1209 Met Asp Asp Asp Asp Leu Arg Arg Gly Leu Pro Thr Cys His Val Lys
W--> 1210          90          95          100
E--> 1212 ttt ggc gaa gca aac gcg att ctc gct ggc gac gct tta caa acg ctg
1213 809
1215 Phe Gly Glu Ala Asn Ala Ile Leu Ala Gly Asp Ala Leu Gln Thr Leu
W--> 1216          105          110          115          120
E--> 1218 gcg ttc tcg att tta agc gat gcc gat atg ccg gaa gtg tcg gac cgc
1219 857
1221 Ala Phe Ser Ile Leu Ser Asp Ala Asp Met Pro Glu Val Ser Asp Arg
W--> 1222          125          130          135
E--> 1224 gac aga att tcg atg att tct gaa ctg gcg agc gcc agt ggt att gcc
1225 905
1227 Asp Arg Ile Ser Met Ile Ser Glu Leu Ala Ser Ala Ser Gly Ile Ala
W--> 1228          140          145          150
E--> 1230 gga atg tgc ggt ggt cag gca tta gat tta gac gcg gaa ggc aaa cac
1231 953
1233 Gly Met Cys Gly Gly Gln Ala Leu Asp Leu Asp Ala Glu Gly Lys His

```

Same

RAW SEQUENCE LISTING

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\1673198.raw

W--> 1234 155 160 165
 E--> 1236 gta cct ctg gac gcg ctt gag cgt att cat cgt cat aaa acc ggc gca
 1237 1001
 1239 Val Pro Leu Asp Ala Leu Glu Arg Ile His Arg His Lys Thr Gly Ala
 W--> 1240 170 175 180
 E--> 1242 ttg att cgc gcc gcc gtt cgc ctt ggt gca tta agc gcc gga gat aaa
 1243 1049
 1245 Leu Ile Arg Ala Ala Val Arg Leu Gly Ala Leu Ser Ala Gly Asp Lys
 W--> 1246 185 190 195 200
 E--> 1248 gga cgt cgt gct ctg ccg gta ctc gac aag tat gca gag agc atc ggc
 1249 1097
 1251 Gly Arg Arg Ala Leu Pro Val Leu Asp Lys Tyr Ala Glu Ser Ile Gly
 W--> 1252 205 210 215
 E--> 1254 ctt gcc ttc cag gtt cag gat gac atc ctg gat gtg gtg gga gat act
 1255 1145
 1257 Leu Ala Phe Gln Val Gln Asp Asp Ile Leu Asp Val Val Gly Asp Thr
 W--> 1258 220 225 230
 E--> 1260 gca acg ttg gga aaa cgc cag ggt gcc gac cag caa ctt ggt aaa agt
 1261 1193
 1263 Ala Thr Leu Gly Lys Arg Gln Gly Ala Asp Gln Gln Leu Gly Lys Ser
 W--> 1264 235 240 245
 E--> 1266 acc tac cct gca ctt ctg ggt ctt gag caa gcc cgg aag aaa gcc cgg
 1267 1241
 1269 Thr Tyr Pro Ala Leu Leu Gly Leu Glu Gln Ala Arg Lys Lys Ala Arg
 W--> 1270 250 255 260
 E--> 1272 gat ctg atc gac gat gcc cgt cag tcg ctg aaa caa ctg gct gaa cag
 1273 1289
 1275 Asp Leu Ile Asp Asp Ala Arg Gln Ser Leu Lys Gln Leu Ala Glu Gln
 W--> 1276 265 270 275 280
 E--> 1278 tca ctc gat acc tcg gca ctg gaa gcg cta gcg gac tac atc atc cag
 1279 1337
 1281 Ser Leu Asp Thr Ser Ala Leu Glu Ala Leu Ala Asp Tyr Ile Ile Gln
 W--> 1282 285 290 295
 E--> 1284 cgt aat aaa taaacaataa gtattaatag gccctg atg agt ttt gat att gcc
 1285 1391
 1287 Arg Asn Lys Met Ser Phe Asp Ile Ala
 W--> 1288 1 5
 E--> 1290 aaa tac ccg acc ctg gca ctg gtc gac tcc acc cag gag tta cga ctg
 1291 1439
 1293 Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser Thr Gln Glu Leu Arg Leu
 W--> 1294 10 15 20
 E--> 1296 ttg ccg aaa gag agt tta ccg aaa ctc tgc gac gaa ctg cgc cgc tat
 1297 1487
 1299 Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys Asp Glu Leu Arg Arg Tyr
 W--> 1300 25 30 35
 E--> 1302 tta ctc gac agc gtg agc cgt tcc agc ggg cac ttc gcc tcc ggg ctg
 1303 1535
 1305 Leu Leu Asp Ser Val Ser Arg Ser Ser Gly His Phe Ala Ser Gly Leu
 W--> 1306 40 45 50

RAW SEQUENCE LISTING

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

```

E--> 1308 ggc acg gtc gaa ctg acc gtg gcg ctg cac tat gtc tac aac acc ccg
      1309 1583
      1311 Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr Val Tyr Asn Thr Pro
W--> 1312 55          60          65          70
E--> 1314 ttt gac caa ttg att tgg gat gtg ggg cat cag gct tat ccg cat aaa
      1315 1631
      1317 Phe Asp Gln Leu Ile Trp Asp Val Gly His Gln Ala Tyr Pro His Lys
W--> 1318          75          80          85
E--> 1320 att ttg acc gga cgc cgc gac aaa atc ggc acc atc cgt cag aaa ggc
      1321 1679
      1322 Ile Leu Thr Thr Gly Arg Arg Asp Lys Ile Gly Thr Ile Arg Gln Lys Gly
W--> 1323          90          95          100
E--> 1325 ggt ctg cac ccg ttc ccg tgg cgc ggc gaa agc gaa tat gac gta tta
      1326 1727
      1328 Gly Leu His Pro Phe Pro Trp Arg Gly Glu Ser Glu Tyr Asp Val Leu
W--> 1329          105          110          115
E--> 1331 agc gtc ggg cat tca tca acc tcc atc agt gcc gga att ggt att gcg
      1332 1775
      1334 Ser Val Gly His Ser Ser Thr Ser Ile Ser Ala Gly Ile Gly Ile Ala
W--> 1335          120          125          130
E--> 1337 gtt gct gcc gaa aaa gaa ggc aaa aat cgc cgc acc gtc tgt gtc att
      1338 1823
      1340 Val Ala Ala Glu Lys Glu Gly Lys Asn Arg Arg Thr Val Cys Val Ile
W--> 1341 135          140          145          150
E--> 1344 ggc gat ggc gcg att acc gca ggc atg gcg ttt gaa gcg atg aat cac
      1345 1871
      1347 Gly Asp Gly Ala Ile Thr Ala Gly Met Ala Phe Glu Ala Met Asn His
W--> 1348          155          160          165
E--> 1350 gcg ggc gat atc cgt cct gat atg ctg gtg att ctc aac gac aat gaa
      1351 1919
      1353 Ala Gly Asp Ile Arg Pro Asp Met Leu Val Ile Leu Asn Asp Asn Glu
W--> 1354          170          175          180
E--> 1356 atg tcg att tcc gaa aat gtc ggc gcg ctc aac aac cat ctg gca cag
      1357 1967
      1359 Met Ser Ile Ser Glu Asn Val Gly Ala Leu Asn Asn His Leu Ala Gln
W--> 1360          185          190          195
E--> 1362 ctg ctt tcc ggt aag ctt tac tct tca ctg cgc gaa ggc ggg aaa aaa
      1363 2015
      1365 Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu Arg Glu Gly Gly Lys Lys
W--> 1366          200          205          210
E--> 1368 gtt ttc tct ggc gtg ccg cca att aaa gag ctg ctc aaa cgc acc gaa
      1369 2063
      1371 Val Phe Ser Gly Val Pro Pro Ile Lys Glu Leu Leu Lys Arg Thr Glu
W--> 1372 215          220          225          230
E--> 1374 gaa cat att aaa ggc atg gta gtg cct ggc acg ttg ttt gaa gag ctg
      1375 2111
      1377 Glu His Ile Lys Gly Met Val Val Pro Gly Thr Leu Phe Glu Glu Leu
W--> 1378          235          240          245
E--> 1380 ggc ttt aac tac atc ggc ccg gtg gac ggt cac gat gtg ctg ggg ctt

```

RAW SEQUENCE LISTING

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

```

1381 2159
1383 Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly His Asp Val Leu Gly Leu
W--> 1384          250          255          260
E--> 1386 atc acc acg cta aag aac atg cgc gac ctg aaa ggc ccg cag ttc ctg
1387 2207
1389 Ile Thr Thr Leu Lys Asn Met Arg Asp Leu Lys Gly Pro Gln Phe Leu
W--> 1390          265          270          275
E--> 1392 cat atc atg acc aaa aaa ggt cgt ggt tat gaa ccg gca gaa aaa gac
1393 2255
1395 His Ile Met Thr Lys Lys Gly Arg Gly Tyr Glu Pro Ala Glu Lys Asp
W--> 1396          280          285          290
E--> 1398 ccg atc act ttc cac gcc gtg cct aaa ttt gat ccc tcc agc ggt tgt
1399 2303
1401 Pro Ile Thr Phe His Ala Val Pro Lys Phe Asp Pro Ser Ser Gly Cys
W--> 1402 295          300          305          310
E--> 1404 ttg ccg aaa agt agc ggc ggt ttg ccg agc tat tca aaa atc ttt ggc
1405 2351
1407 Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser Tyr Ser Lys Ile Phe Gly
W--> 1408          315          320          325
E--> 1410 gac tgg ttg tgc gaa acg gca gcg aaa gac aac aag ctg atg gcg att
1411 2399
1413 Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp Asn Lys Leu Met Ala Ile
W--> 1414          330          335          340
E--> 1416 act ccg gcg atg cgt gaa ggt tcc gcc atg gtc gag ttt tca cgt aaa
1417 2447
1419 Thr Pro Ala Met Arg Glu Gly Ser Gly Met Val Glu Phe Ser Arg Lys
W--> 1420          345          350          355
E--> 1422 ttc ccg gat cgc tac ttc gac gtg gca att gcc gag caa cac gcg gtg
1423 2495
1425 Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile Ala Glu Gln His Ala Val
W--> 1426          360          365          370
E--> 1428 acc ttt gct gcg ggt ctg gcg att ggt ggg tac aaa ccc att gtc gcg
1429 2543
1431 Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly Tyr Lys Pro Ile Val Ala
W--> 1432 375          380          385          390
E--> 1434 att tac tcc act ttc ctg caa cgc gcc tat gat cag gtg ctg cat gac
1435 2591
1437 Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln Val Leu His Asp
W--> 1438          395          400          405
E--> 1440 gtg gcg att caa aag ctt ccg gtc ctg ttc gcc atc gac cgc gcg ggc
1441 2639
1443 Val Ala Ile Gln Lys Leu Pro Val Leu Phe Ala Ile Asp Arg Ala Gly
W--> 1444          410          415          420
E--> 1446 att gtt ggt gct gac ggt caa acc cat cag ggt gct ttt gat ctc tct
1447 2687
1449 Ile Val Gly Ala Asp Gly Gln Thr His Gln Gly Ala Phe Asp Leu Ser
W--> 1450          425          430          435
E--> 1452 tac ctg cgc tgc ata ccg gaa atg gtc att atg acc ccg agc gat gaa
1453 2735

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,198

DATE: 12/26/2000

TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

1455 Tyr Leu Arg Cys Ile Pro Glu Met Val Ile Met Thr Pro Ser Asp Glu
 W--> 1456 440 445 450
 E--> 1458 aac gaa tgt cgc cag atg ctc tat acc ggc tat cac tat aac gat ggc
 1459 2783
 1461 Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly Tyr His Tyr Asn Asp Gly
 W--> 1462 455 460 465 470
 E--> 1464 ccg tca gcg gtg cgc tac ccg cgt ggc aac gcg gtc ggc gtg gaa ctg
 1465 2831
 1467 Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn Ala Val Gly Val Glu Leu
 W--> 1468 475 480 485
 E--> 1470 acg ccg ctg gaa aaa cta cca att ggc aaa ggc att gtg aag cgt cgt
 1471 2879
 1473 Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys Gly Ile Val Lys Arg Arg
 W--> 1474 490 495 500
 E--> 1476 ggc gag aaa ctg gcg atc ctt aac ttt ggt acg ctg atg cca gaa gcg
 1477 2927
 1479 Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly Thr Leu Met Pro Glu Ala
 W--> 1480 505 510 515
 E--> 1482 gcg aaa gtc gcc gaa tcg ctg aac gcc acg ctg gtc gat atg cgt ttt
 1483 2975
 1485 Ala Lys Val Ala Glu Ser Leu Asn Ala Thr Leu Val Asp Met Arg Phe
 W--> 1486 520 525 530
 E--> 1488 gtg aaa ccg ctt gat gaa gcg tta att ctg gaa atg gcc gcc agc cat
 1489 3023
 1491 Val Lys Pro Leu Asp Glu Ala Leu Ile Leu Glu Met Ala Ala Ser His
 W--> 1492 535 540 545 550
 E--> 1494 gaa gcg ctg gtc acc gta gaa gaa aac gcc att atg ggc ggc gca ggc
 1495 3071
 1497 Glu Ala Leu Val Thr Val Glu Glu Asn Ala Ile Met Gly Gly Ala Gly
 W--> 1498 555 560 565
 E--> 1500 agc ggc gtg aac gaa gtg ctg atg gcc cat cgt aaa cca gta ccc gtg
 1501 3119
 1503 Ser Gly Val Asn Glu Val Leu Met Ala His Arg Lys Pro Val Pro Val
 W--> 1504 570 575 580
 E--> 1506 ctg aac att ggc ctg ccg gac ttc ttt att ccg caa gga act cag gaa
 1507 3167
 1509 Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile Pro Gln Gly Thr Gln Glu
 W--> 1510 585 590 595
 E--> 1512 gaa atg cgc gcc gaa ctc ggc ctc gat gcc gct ggt atg gaa gcc aaa
 1513 3215
 1515 Glu Met Arg Ala Glu Leu Gly Leu Asp Ala Ala Gly Met Glu Ala Lys
 W--> 1516 600 605 610
 E--> 1518 atc aag gcc tgg ctg gca taatccctac tccactcctg ctatgcttaa
 1519 3263
 1521 Ile Lys Ala Trp Leu Ala
 W--> 1522 615 620
 E--> 1524 gaaattatc atagactcta aataattcga gttgcaggaa ggccggcaaac gagtgaagcc
 1525 3323
 E--> 1528 ccaggagctt acataagtaa gtg act ggg gtg aac gaa tgc agc cgc agc aca

RAW SEQUENCE LISTING DATE: 12/26/2000
 PATENT APPLICATION: US/09/673,198 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
 Output Set: N:\CRF3\12262000\I673198.raw

```

1529 3376
1531          Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr
W--> 1532          1          5          10
E--> 1534 tgc aac ttg aag tat gac gag tat agc agg agt ggc agc atg caa tac
1535 3424
1537 Cys Asn Leu Lys Tyr Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr
W--> 1538          15          20          25
E--> 1540 aac ccc tta gga aaa acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc
1541 3472
1543 Asn Pro Leu Gly Lys Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly
W--> 1544          30          35          40
E--> 1546 tgt atg acc ttt ggc gag cca gat cgc ggt aat cac gca tgg aca ctg
1547 3520
1549 Cys Met Thr Phe Gly Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu
W--> 1550          45          50          55
E--> 1552 ccg gaa gaa agc agc cgt ccc ata att aaa cgt gca ctg gaa ggc ggc
1553 3568
1555 Pro Glu Glu Ser Ser Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Gly
W--> 1556          60          65          70          75
E--> 1558 ata aat ttc ttt gat acc gcc aac agt tat tct gac ggc agc agc gaa
1559 3616
1561 Ile Asn Phe Phe Asp Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu
W--> 1562          80          85          90
E--> 1564 gag atc gtc ggt cgc gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg
1565 3664
1567 Glu Ile Val Gly Arg Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val
W--> 1568          95          100          105
E--> 1570 gtc gtt gcg acc aaa gtg ttc cat cgc gtt ggt gat tta ccg gaa gga
1571 3712
1573 Val Val Ala Thr Lys Val Phe His Arg Val Gly Asp Leu Pro Glu Gly
W--> 1574          110          115          120
E--> 1575 tta tcc cgt gcg caa att ttg cgc tct atc gac gac agc ctg cga cgt
1576 3760
1578 Leu Ser Arg Ala Gln Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg
W--> 1579          125          130          135
E--> 1581 ctc ggc atg gat tat gtc gat atc ctg caa att cat cgc tgg gat tac
1582 3808
1584 Leu Gly Met Asp Tyr Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr
W--> 1585          140          145          150          155
E--> 1587 aac acg ccg atc gaa gag acg ctg gaa gcc ctc aac gac gtg gta aaa
1588 3856
1590 Asn Thr Pro Ile Glu Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys
W--> 1591          160          165          170
E--> 1593 gcc ggg aaa gcg cgt tat atc ggc gcg tca tca atg cac gct tcg cag
1594 3904
1596 Ala Gly Lys Ala Arg Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln
W--> 1597          175          180          185
E--> 1599 ttt gct cag gca ctg gaa ctc caa aaa cag cac ggc tgg gcg cag ttt
1600 3952

```

same

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/673,198
 DATE: 12/26/2000
 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
 Output Set: N:\CRF3\12262000\1673198.raw

1602 Phe Ala Gln Ala Leu Gln Leu Gln Lys Gln His Gly Trp Ala Gln Phe
 W--> 1603 190 195 200
 E--> 1605 gtc agt atg cag gat cac tac aat ctg att tat cgt gaa gaa gag cgc
 1606 4000
 1608 Val Ser Met Gln Asp His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg
 W--> 1609 205 210 215
 E--> 1611 gag atg cta cca ctg tgt tat cag gag ggc gtg gcg gta att cca tgg
 1612 4048
 1614 Glu Met Leu Pro Leu Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp
 W--> 1615 220 225 230 235
 E--> 1617 agc ccg ctg gca agg ggc cgt ctg acg cgt ccg tgg gga gaa act acc
 1618 4096
 1620 Ser Pro Leu Ala Arg Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr
 W--> 1621 240 245 250
 E--> 1623 gca cga ctg gtg tct gat gag gtg ggg aaa aat ctc tat aaa gaa agc
 1624 4144
 1626 Ala Arg Leu Val Ser Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser
 W--> 1627 255 260 265
 E--> 1629 gat gaa aat gac gcg cag atc gca gag cgg tta aca gcc gtc agt gaa
 1630 4192
 1632 Asp Glu Asn Asp Ala Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu
 W--> 1633 270 275 280
 E--> 1635 gaa ctg ggg gcg aca cga gca caa gtt gcg ctg gcc tgg ttg ttg agt
 1636 4240
 1638 Glu Leu Gly Ala Thr Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser
 W--> 1639 285 290 295
 E--> 1641 aaa ccg gcc att gcc gca ccg att atc gga act tcg cgc gaa gaa cag
 1642 4288
 1644 Lys Pro Gly Ile Ala Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln
 W--> 1645 300 305 310 315
 E--> 1647 ctt gat gag cta ttg aac gcg gtg gat atc act ttg aag ccg gaa cag
 1648 4336
 1650 Leu Asp Glu Leu Leu Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln
 W--> 1651 320 325 330
 E--> 1653 att gcc gaa ctg gaa acg ccg tat aaa ccg cat cct gtc gta gga ttt
 1654 4384
 1656 Ile Ala Glu Leu Glu Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe
 W--> 1657 335 340 345
 E--> 1659 aaa taa
 1660 4390
 1662 Lys
 1665 <210> SEQ ID NO: 12
 1666 <211> LENGTH: 33
 1667 <212> TYPE: DNA
 1668 <213> ORGANISM: Artificial Sequence
 1670 <220> FEATURE:
 1671 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 1673 <400> SEQUENCE: 12
 E--> 1674 ccggatccat ggcggcaatg gttcgttggc aag

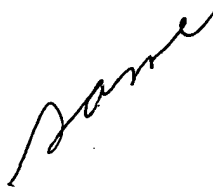
Done

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,198

DATE: 12/26/2000
TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\1673198.raw

1675 33
1679 <210> SEQ ID NO: 13
1680 <211> LENGTH: 34
1681 <212> TYPE: DNA
1682 <213> ORGANISM: Artificial Sequence
1684 <220> FEATURE:
1685 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1687 <400> SEQUENCE: 13
E--> 1688 ccgaattctt atttaaatcc tacgacagga tgcg
1689 34
1693 <210> SEQ ID NO: 14
1694 <211> LENGTH: 33
1695 <212> TYPE: DNA
1696 <213> ORGANISM: Artificial Sequence
1698 <220> FEATURE:
1699 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1701 <400> SEQUENCE: 14
E--> 1702 ccggatccat gagttttgat attgccaaat acc
1703 33
1707 <210> SEQ ID NO: 15
1708 <211> LENGTH: 33
1709 <212> TYPE: DNA
1710 <213> ORGANISM: Artificial Sequence
1712 <220> FEATURE:
1713 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1715 <400> SEQUENCE: 15
E--> 1716 ccgaattctt atgccagcca ggccttgatt ttg
1717 33
1721 <210> SEQ ID NO: 16
1722 <211> LENGTH: 33
1723 <212> TYPE: DNA
1724 <213> ORGANISM: Artificial Sequence
1726 <220> FEATURE:
1727 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1729 <400> SEQUENCE: 16
E--> 1730 ccgaattctt actcattgtc cgggtgtaaaa ggg
1731 33
1735 <210> SEQ ID NO: 17
1736 <211> LENGTH: 33
1737 <212> TYPE: DNA
1738 <213> ORGANISM: Artificial Sequence
1740 <220> FEATURE:
1741 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1743 <400> SEQUENCE: 17
E--> 1744 ccggatccat ggactttccg cagcaactcg aag
1745 33
1749 <210> SEQ ID NO: 18
1750 <211> LENGTH: 33
1751 <212> TYPE: DNA



RAW SEQUENCE LISTING DATE: 12/26/2000
 PATENT APPLICATION: US/09/673,198 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
 Output Set: N:\CRF3\12262000\I673198.raw

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1752 <213> ORGANISM: Artificial Sequence
1754 <220> FEATURE:
1755 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1757 <400> SEQUENCE: 18
E--> 1758 ccgaattctt atttattacg ctggatgatg tag
1759 33
1763 <210> SEQ ID NO: 19
1764 <211> LENGTH: 33
1765 <212> TYPE: DNA
1766 <213> ORGANISM: Artificial Sequence
1768 <220> FEATURE:
1769 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1771 <400> SEQUENCE: 19
E--> 1772 ccggatccta atccctactc cactcctgct atg
1773 33
1777 <210> SEQ ID NO: 20
1778 <211> LENGTH: 30
1779 <212> TYPE: DNA
1780 <213> ORGANISM: Artificial Sequence
1782 <220> FEATURE:
1783 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1785 <400> SEQUENCE: 20
E--> 1786 gggggatcca agcaactcac cattctgggc
1787 30
1791 <210> SEQ ID NO: 21
1792 <211> LENGTH: 30
1793 <212> TYPE: DNA
1794 <213> ORGANISM: Artificial Sequence
1796 <220> FEATURE:
1797 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1799 <400> SEQUENCE: 21
E--> 1800 gggggatccg cttgcgagac gcacacctc
1801 30
1805 <210> SEQ ID NO: 22
1806 <211> LENGTH: 32
1807 <212> TYPE: DNA
1808 <213> ORGANISM: Artificial Sequence
1810 <220> FEATURE:
1811 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1813 <400> SEQUENCE: 22
E--> 1814 gggggatcca gttttgatat tyccaaatac cc
1815 32
1819 <210> SEQ ID NO: 23
1820 <211> LENGTH: 32
1821 <212> TYPE: DNA
1822 <213> ORGANISM: Artificial Sequence
1824 <220> FEATURE:
1825 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1827 <400> SEQUENCE: 23

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Same

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,198

DATE: 12/26/2000
TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt
Output Set: N:\CRF3\12262000\I673198.raw

E--> 1828 gggggatcct gccagccagg ccttgatttt gg
1829 32
1833 <210> SEQ ID NO: 24
1834 <211> LENGTH: 30
1835 <212> TYPE: DNA
1836 <213> ORGANISM: Artificial Sequence
1838 <220> FEATURE:
1839 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1841 <400> SEQUENCE: 24
E--> 1842 gggggatccg agcaactcac cattctgggc
1843 30
1847 <210> SEQ ID NO: 25
1848 <211> LENGTH: 30
1849 <212> TYPE: DNA
1850 <213> ORGANISM: Artificial Sequence
1852 <220> FEATURE:
1853 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
1855 <400> SEQUENCE: 25
E--> 1856 gggggatccg cttgcgagac gcacacctc
1857 30

same

VERIFICATION SUMMARY

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:36

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

L:9 M:201 W: Mandatory field data missing, FILE REFERENCE
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:402 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:6
M:254 Repeated in SeqNo=6
L:647 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:7
M:254 Repeated in SeqNo=7
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:8
M:254 Repeated in SeqNo=8
L:813 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:9
M:254 Repeated in SeqNo=9
L:956 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:10
M:254 Repeated in SeqNo=10
L:1128 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
M:254 Repeated in SeqNo=11
L:1173 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11
L:1174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:1360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

VERIFICATION SUMMARY

DATE: 12/26/2000

PATENT APPLICATION: US/09/673,198

TIME: 13:19:36

Input Set : A:\1241.16 sequence.txt

Output Set: N:\CRF3\12262000\I673198.raw

L:1366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1420 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1426 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
 L:1674 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:12
 L:1688 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:13
 L:1702 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:14
 L:1716 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:15
 L:1730 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:16
 L:1744 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:17
 L:1758 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18
 L:1772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:19
 L:1786 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:20
 L:1800 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:21
 L:1814 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:22
 L:1828 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:23
 L:1842 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:24
 L:1856 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:25
 L:1997 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:27
 M:254 Repeated in SeqNo=27
 L:2338 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:29
 M:254 Repeated in SeqNo=29
 L:2636 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:31
 M:251 Repeated in SeqNo=31
 L:2771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:32
 L:2784 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:33
 L:2797 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:34